

## SEQUENCE LISTING

<110> MIYAWAKI, Atsushi  
ANDU, Ryoko  
KARASAWA, Satoshi  
MIZUNO, Hideaki

<120> FLUORESCENT PROTEIN AND CHROMOPROTEIN

<130> P26794

<140> US 10/525,365  
<141> 2005-02-23

<150> JP2002/243337  
<151> 2002-08-23

<150> JP2002/243338  
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<150> JP2002/274266  
<151> 2002-09-20

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<170> PatentIn version 3.3

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Lys Pro Phe Glu Gly Tyr Gln Val Glu Lys Ile Arg Val Thr Glu Gly  
 35 40 45

Gly Pro Leu Pro Phe Ala Tyr Asp Thr Leu Thr Pro Cys Trp Met Tyr  
 50 55 60

Gly Ser Lys Thr Phe Ile Lys His Thr Ser Gly Ile Pro Asp Tyr Phe  
 65 70 75 80

Lys Glu Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Gln Ile Tyr  
 85 90 95

Glu Asp Gly Gly Cys Leu Thr Ile His Gln Asp Thr Ser Met Gln Gly  
 100 105 110

Asp Cys Phe Ile Phe Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala  
 115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Ala Gly Trp Glu Pro Cys Val  
 130 135 140

Glu Met Leu Tyr Pro Arg Ala Gly Val Leu Cys Gly Gln Ser Leu Met  
 145 150 155 160

Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr  
 165 170 175

Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe  
 180 185 190

Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg  
 195 200 205

Ile Glu Gln Tyr Glu Ala Ala Val Ala Arg Tyr Cys Glu Ala Pro Ser  
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Arg Leu Gly His His  
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<213> *Anthopleura inornata*

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120

gaaaagatta gagttactga aggaggtccg ctaccctttg cgtacgatac tttgacacct  
180

tgctggatgt atggaagtaa aaccttcac aagcatacat caggaattcc cgattacttc  
240

aaggagtctc ttctgaagg ctttacttgg gaaagaacgc aaatctacga ggatggaggc  
300

tgtcttacta ttcaccagga cacaagcatg caggagatt gttttatattt caagataaaa  
360

gtcattggta ccaactttcc tgccaatggc cccgtgatgc agaagaaaac agcaggatgg  
420

gagccatgcg ttgagatgct ttatcctcgt gccggtgtct tgtgtggaca gtcgttgatg  
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gccctgaaat gcaaggatgg caaccacctg acgtgccatc tgcgaactac ctacagggtcc  
540

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Lys Pro Phe Glu Gly Tyr Gln Val Glu Lys Ile Arg Val Thr Glu Gly  
 35 40 45

Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Ala Pro Cys Cys Ser Tyr  
 50 55 60

Gly Ser Lys Thr Phe Ile Lys His Val Ser Gly Ile Pro Asp Tyr Phe  
 65 70 75 80

Lys Glu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Gln Ile Tyr  
 85 90 95

Glu Asp Gly Gly Ser Leu Ser Ile His Gln Asp Thr Ser Leu Gln Gly  
 100 105 110

Asp Cys Phe Ile Tyr Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala  
 115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Ala Gly Trp Glu Pro Cys Val  
 130 135 140

Glu Met Leu Tyr Pro Arg Ala Gly Val Leu Cys Gly Gln Ser Leu Met  
 145 150 155 160

Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr  
 165 170 175

Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe  
                   180                                  185                                  190

Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg  
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Ile Glu Gln Tyr Glu Ala Ala Val Ala Arg Tyr Cys Glu Ala Pro Ser  
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Arg Leu Gly His His  
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gaaaagatta gagttactga aggaggtccg ctaccctttg cgtacgatat tttggcacct  
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tgctgctcgt atggaagtaa aaccttcac c aagcatgtct cggaatccc cgattacttc  
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aaggagtcct tccctgaagg ctttacttgg gaaagaacgc aaatctacga ggatggaggc  
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540

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<213> Trachyphyllia geoffroyi

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			20					25					30		

Pro	Phe	Glu	Gly	Lys	Gln	Ser	Met	Asp	Leu	Val	Val	Lys	Glu	Gly	Ala
		35					40					45			

Pro	Leu	Pro	Phe	Ala	Tyr	Asp	Ile	Leu	Thr	Thr	Ala	Phe	His	Tyr	Gly
	50					55					60				

Asn	Arg	Val	Phe	Ala	Lys	Tyr	Pro	Asp	His	Ile	Pro	Asp	Tyr	Phe	Lys
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Gln	Ser	Phe	Pro	Lys	Gly	Phe	Ser	Trp	Glu	Arg	Ser	Leu	Met	Phe	Glu
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Asp	Gly	Gly	Val	Cys	Ile	Ala	Thr	Asn	Asp	Ile	Thr	Leu	Lys	Gly	Asp
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Thr Phe Phe Asn Lys Val Arg Phe Asp Gly Val Asn Phe Pro Pro Asn  
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Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Ala Ser Thr Glu  
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Lys Met Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Ile Thr Met Ala  
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Leu Leu Leu Lys Gly Asp Val His Tyr Arg Cys Asp Phe Arg Thr Thr  
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Tyr Lys Ser Arg Gln Glu Gly Val Lys Leu Pro Gly Tyr His Phe Val  
                                   180                                  185                                  190

Asp His Cys Ile Ser Ile Leu Arg His Asp Lys Asp Tyr Asn Glu Val  
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Lys Leu Tyr Glu His Ala Val Ala His Ser Gly Leu Pro Asp Asn Val  
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           120

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240

cagtcgtttc ccaaagggtt ttcttgggag cgaagcctga tgttcgagga cgggggcggt  
300

tgcatcgcta caaatgacat aacactgaaa ggagacactt tttttaacaa agttcgattt  
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420

gcatccactg agaaaatgta tttgcgtgat ggagtgttga cgggcgatat taccatggct  
480

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540

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&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Trachyphyllia geoffroyi

&lt;400&gt; 7

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Asn	Val	Asn	Gly	His	Gln	Phe	Val	Ile	Glu	Gly	Asp	Gly	Lys	Gly	His
			20					25					30		

Pro	Phe	Glu	Gly	Lys	Gln	Ser	Met	Asp	Leu	Val	Val	Lys	Glu	Gly	Ala
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Pro	Leu	Pro	Phe	Ala	Tyr	Asp	Ile	Leu	Thr	Thr	Ala	Phe	His	Tyr	Gly
	50					55					60				



Asn Arg Val Phe Ala Lys Tyr Pro Asp His Ile Pro Asp Tyr Phe Lys  
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Gln Ser Phe Pro Lys Gly Phe Ser Trp Glu Arg Ser Leu Met Phe Glu  
85 90 95

Asp Gly Gly Val Cys Ile Ala Thr Asn Asp Ile Thr Leu Lys Gly Asp  
100 105 110

Thr Phe Phe Asn Lys Val Arg Phe Asp Gly Val Asn Phe Pro Pro Asn  
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Ala Ser Thr Glu  
130 135 140

Lys Met Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Ile Arg Met Glu  
145 150 155 160

Leu Leu Leu Lys Gly Asp Val His Tyr Arg Cys Asp Phe Arg Thr Thr  
165 170 175

Tyr Lys Ser Arg Gln Glu Gly Val Lys Leu Pro Gly Tyr His Phe Val  
180 185 190

Asp His Cys Ile Ser Ile Leu Arg His Asp Lys Asp Tyr Asn Glu Val  
195 200 205

Lys Leu Tyr Glu His Ala Val Ala His Ser Gly Leu Pro Asp Asn Val  
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<213> *Trachyphyllia geoffroyi*

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ttccattatg gtaacagggt ttttgctaaa taccagacc atataccaga ctacttcaag  
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360

gatggcgtaa actttcccc aaatggtcct gttatgcaga agaagactct gaaatgggag  
420

gcacccactg agaaaatgta tttgcgtgat ggagtgttga cgggcgatat taggatggag  
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 35 40 45  
 Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr  
 50 55 60  
 Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe  
 65 70 75 80  
 Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe  
 85 90 95  
 Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly  
 100 105 110  
 Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro  
 115 120 125  
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr  
 130 135 140  
 Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met  
 145 150 155 160  
 Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr  
 165 170 175  
 Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe  
 180 185 190

Ile Asp His Cys Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn  
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Glu Lys Gln Gln Gln  
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           600

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35 40 45

Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr  
50 55 60

Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe  
65 70 75 80

Glu Gln Ser Phe Pro Lys Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe  
85 90 95

Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Glu Gly  
100 105 110

Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro  
115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Pro Ser Thr  
130 135 140

Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met  
 145 150 155 160

Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr  
 165 170 175

Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe  
 180 185 190

Ile Asp His Cys Ile Glu Ile Leu Ser His His Asn Asp Tyr Asn Asn  
 195 200 205

Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys  
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Glu Lys Gln Gln Gln  
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 180

gcattccatt acggcaaccg ggtattcgcc aaatacccaa aggatatacc aaactatttc  
 240

gagcagtcgt ttcctaaggg gtattcgtgg gaacggagca tgattttcga agacgggggc  
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360

ttttatggtg taaacttccc cccaatggt ccagttatgc agaagaagac gcagaagtgg  
420

gagccatcca ctgagaaaat gtatgcgcgt gatggagtgt tgacgggtga tattaacatg  
480

gctctgttgc ttaaaggggg tggccattac cgatgtgact tcagaactac tttcaaagct  
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aaggagaagg gtgtcaagtt gccaggctac cactttatag atcactgcat agagatttta  
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690

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&lt;211&gt; 229

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&lt;213&gt; Scolymia vitiensis

&lt;400&gt; 13

Met Val Ser Val Ile Lys Asp Glu Met Lys Val Asn Leu Arg Met Glu  
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Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Leu Gly Ser Gly  
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Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly  
35 40 45

Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr  
50 55 60

Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe  
65 70 75 80

Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe  
85 90 95

Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly  
100 105 110

Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro  
115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr  
130 135 140

Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met  
145 150 155 160

Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr  
165 170 175

Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe  
180 185 190

Ile Asp His Cys Met Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn  
195 200 205

Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys  
210 215 220

Glu Lys Gln Gln Gln  
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<212> DNA

<213> Scolymia vitiensis

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120

attgagctta aagtcgtaaa ggggtggacct ttacctttcg cctacgatat cctgacaaca  
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gcattccatt acggcaaccg ggtattcgcc aaatacccaa aggatatacc aaactatttc  
240

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ttttatgggtg taaatttccc cccaatggg ccagttatgc agaagaagac gcagaaatgg  
420

gagcaatcca ctgagaaaat gtatgcgcgt gatggagtgt tgacgggtga tattaacatg  
480

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660

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<213> Scolymia vitiensis

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			20					25					30		

Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly  
 35 40 45

Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr  
 50 55 60

Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe  
 65 70 75 80

Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe  
 85 90 95

Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly  
 100 105 110

Gly Thr Phe Tyr Asn Lys Val Arg Phe Glu Gly Val Asn Phe Pro Pro  
 115 120 125

Asn Gly Pro Val Met Gln Lys Asn Thr Leu Lys Trp Glu Pro Ser Thr  
 130 135 140

Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met  
 145 150 155 160

Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr  
 165 170 175

Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr  
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Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn  
 195 200 205

Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp  
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 180

gcattccatt acggcaaccg ggtattcgcc aaatacccaa aggatatacc aaactatttc  
 240

gagcagtcgt ttcctgaggg gtattcgtgg gaacggagca tgattttcga agacgggggc  
 300

atttgcacgc ctagaaacga cataacaatg gatggtggca ctttctataa taaagttcga  
 360

tttgaaggtg taaatttccc cccaatggt ccagttatgc agaagaatac gctgaaatgg  
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gagccatcca ctgagaaaat gtatgcgcgt gatggagtgt tgacgggtga tattgacatg  
 480

tcctgttgc ttaaaggggg tggccattac cgatgtgact tcagaactac tttcaaagct  
 540

aaggagaagg gtgtcaagtt gccaggcacc cactacatag atcacagcat agagatttta  
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ttgcaggact aa  
 672

<210> 17  
 <211> 223  
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&lt;213&gt; Scolymia vitiensis

&lt;400&gt; 17

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Gly	Ser	Val	Asn	Gly	His	Asp	Phe	Val	Ile	Asp	Gly	Thr	Gly	Ser	Gly
			20					25					30		

Lys	Pro	Lys	Glu	Gly	Thr	Gln	Thr	Ile	Glu	Leu	Lys	Val	Val	Lys	Gly
		35					40					45			

Gly	Pro	Leu	Pro	Phe	Ala	Tyr	Asp	Ile	Leu	Thr	Thr	Ala	Phe	His	Tyr
	50					55					60				

Gly	Asn	Arg	Val	Phe	Ala	Lys	Tyr	Pro	Lys	Asp	Ile	Pro	Asn	Tyr	Phe
65					70					75					80

Glu	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Ser	Trp	Glu	Arg	Ser	Met	Thr	Phe
				85					90					95	

Glu	Asp	Gly	Gly	Val	Cys	Thr	Ala	Arg	Asn	Asp	Ile	Thr	Met	Asp	Gly
			100					105					110		

Gly	Thr	Phe	Tyr	Asn	Lys	Val	Arg	Phe	Glu	Gly	Thr	Asn	Phe	Pro	Pro
		115					120					125			

Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Leu	Lys	Trp	Glu	Pro	Ser	Thr
	130					135					140				

Glu	Lys	Met	Tyr	Ala	Arg	Asp	Gly	Val	Leu	Thr	Gly	Asp	Ile	Asp	Met
145					150					155					160

Ser	Leu	Leu	Leu	Lys	Gly	Gly	Gly	His	Tyr	Arg	Cys	Asp	Met	Arg	Thr
				165					170					175	

Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr  
 180 185 190

Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn  
 195 200 205

Val Thr Leu Tyr Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp  
 210 215 220

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ggacacgact tcgtgattga cggaactggt tcaggcaagc ctaaagaggg aacacagact  
 120

attgagctta aagtcgtaaa ggggtggacct ttacctttcg cctacgatat cctgacaaca  
 180

gcattccatt acggcaaccg ggtattcgcc aaatacccaa aggatatacc aaactatttc  
 240

gagcagtcgt ttcctgaggg gtattcgtgg gaacggagca tgactttcga agacgggggc  
 300

gtttgcaccg ctagaaacga cataacaatg gatgggtggca ctttctataa taaagttcga  
 360

tttgaaggta caaatattccc cccaatggt ccagttatgc agaagaagac gctgaaatgg  
 420

gagccatcca ctgagaaaat gtatgcgcgt gatggagtgt tgacgggtga tattgacatg  
 480

tcctgttgc ttaaaggggg tggccattac cgatgtgaca tgagaactac tttcaaagct  
 540

aaggagaagg gtgtcaagtt gccaggcacc cactacatag atcacagcat agagatttta  
 600

agccatcgca acgattacaa caacgttacg ctttatgagc atgctgttgc tcgttctgga  
660

ttgcaggact aa  
672

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<211> 21  
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<220>  
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<220>  
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<222> (18)..(18)  
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21

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<223> v is a, c, or g

<220>

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<223> d is a, g, or t

<220>

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<223> y is c or t

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<222> (12)..(12)

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<220>

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<222> (14)..(14)

<223> v is a, c, or g

<220>

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<222> (21)..(21)

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23

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<220>

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25

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ggccacgcgt cgactagtac  
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aaaatatcgt acgcaaaggg  
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<400> 25  
aggaggtccg ctaccctttg  
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<210> 26  
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<400> 26  
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33

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<220>  
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<222> (21)..(21)

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<210> 29

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<223> primer

<400> 29

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<210> 30

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<212> DNA

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<223> primer

<400> 30

ggccacgcgt cgactagtac  
20

<210> 31

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 31

tcttcgtaag tcatgcttcg ttc

23

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ggtattcgcc aaatacccaa a

21

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<212> DNA

<213> Artificial Sequence

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<400> 33

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<400> 34

ccgctcgagt tggtgttggt tctctttgtc ctg

33